

## SEQUENCE LISTING

<110> Rhone-Poulenc Agro; Betzner, Andreas Stefan; Doutriaux,  
 Marie-Pascale; Freyssinet, Georges; Perez, Pascual.  
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cgacatacta atcacttcca gcgaccaatt tcctgagctt gctgaagctc gccaaagcagt 780

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Met Gly Lys Gln Lys Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys  
1 5 10 15

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Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr  
20 25 30

ccg cca ccg aag ata tcc gcc act gta tcc ttc tct cct tcc aag cgt 243  
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg  
35 40 45

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Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys  
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ctt tct cct cac act caa aac cca gta ccc gat ccc aat tta cac caa 339  
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln  
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 Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val  
                     100                    105                    110

gag cta aag agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt 483  
 Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly  
                     115                    120                    125

tac agg tac aga ttc ttc gga gaa gac gcg gag atc gca gca cgc gtg 531  
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 Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val  
                     145                    150                    155                    160

cca aca ttt cga ttg aat ttc cac gtg aga aga ctg gtg aat gca gga 627  
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 Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser  
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cat ggt gca aac cgg acc ggc cct ttt ttc cgg gga ctg tcg gcg ttg 723  
 His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu  
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tat acc aaa gcc acg ctt gaa gcg gct gag gat ata agt ggt ggt tgt 771  
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gtg gat gag aga gtt aag tcg gag aca tta ggc tgt ggt att gaa atg 867  
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gaa gtt gtt tat gaa gag ttc aat gat aat ttc atg aga agt gga tta 963  
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acc tca aac gtt cga gtg gaa cgt gcc tca ctg gat tgt ttc agc aat	1107	
Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn		
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Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala		
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Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys		
355	360 365	
gga atg tct tgc ttg aca gtt cat aca att atg aac atg cca cat ctg	1251	
Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu		
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gct gtt tct gag att tct gct tgc atg gga tct cat agt tct tcc cag	1587	
Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Ser Gln		
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gag ctt gga aga ggc act agc aca cac gac ggt gta gcc att gcc tat 2835  
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 Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe  
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gtc acg cat tac cct gaa ata gct gag atc agt aac gga ttc cca ggt 2931  
 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly  
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Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg  
 35 40 45

Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys  
 50 55 60

Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln  
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Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro  
 85 90 95

Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val  
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Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly  
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Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val  
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Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val  
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Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly  
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His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu  
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Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys  
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Gly Gly Glu Glu Gly Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val  
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Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met  
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15

Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly  
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 Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp  
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 Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg  
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 Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala  
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		595					600					605			
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	610					615					620				
Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala
625					630					635					640
Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg
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Lys	Lys	Leu	Ala	Ile	Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile
			660					665					670		
Thr	His	Leu	Ile	Glu	Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	His	Asn	Trp
		675					680					685			
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	690					695					700				
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Ile	Val	Asn	Arg	Ala	Ser	Trp	Asp	Ser	Phe	Leu	Lys	Ser	Phe	Ser	Arg
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			740					745					750		
Cys	Leu	His	Ser	Leu	Ser	Thr	Leu	Ser	Arg	Asn	Lys	Asn	Tyr	Val	Arg
		755					760					765			
Pro	Glu	Phe	Val	Asp	Asp	Cys	Glu	Pro	Val	Glu	Ile	Asn	Ile	Gln	Ser
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Gly	Arg	His	Pro	Val	Leu	Glu	Thr	Ile	Leu	Gln	Asp	Asn	Phe	Val	Pro



17

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala  
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Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp  
850 855 860

Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala  
865 870 875 880

Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp  
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900 905 910

Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe  
915 920 925

Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly  
930 935 940

Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys  
945 950 955 960

Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg  
965 970 975

Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln  
980 985 990

Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu  
995 1000 1005

Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro  
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Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro  
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ccgtctggat ttaagccggc tgaatccgcc ggtgatgctt cgtccctgtt ctccaatatt 300

atgcataagt ttgtaaaagt cgatgatcga gattgtttctg gagagaggag ccgagaagat 360

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cgttccaata atggtaaaac tcaagaaaga aacctgctt ttagtttcag tgggagagct 480

gaacttagat cagtagaaga tataggagta gatggcgatg ttcctgggtcc agaaacacca 540

gggatgcgct cacgtgcttc tcgcttgaag cgagttctgg aggatgaaat gacttttaag 600

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tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171  
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23

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Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp	
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Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg	
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gaa ggg gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa	315
Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys	
45 50 55	
tct gtc gat gag gtt aga gga acg gat act cca ccg gag aag gtt ccg	363
Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro	
60 65 70	
cgt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gst gat	411
Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp	
75 80 85 90	
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Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp	
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Asp Arg Asp Cys Ser Gly Glu Arg Ser Arg Glu Asp Val Val Pro Leu	
110 115 120	
aat gat tca tct cta tgt atg aag gct aat gat gtt att cct caa ttt	555
Asn Asp Ser Ser Leu Cys Met Lys Ala Asn Asp Val Ile Pro Gln Phe	
125 130 135	
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Arg Ser Asn Asn Gly Lys Thr Gln Glu Arg Asn His Ala Phe Ser Phe	
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Ser Gly Arg Ala Glu Leu Arg Ser Val Glu Asp Ile Gly Val Asp Gly	
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Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg	
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Leu Lys Arg Val Leu Glu Asp Glu Met Thr Phe Lys Glu Asp Lys Val	
190 195 200	
cct gta ttg gac tct aac aaa agg ctg aaa atg ctc cag gat ccg gtt	795
Pro Val Leu Asp Ser Asn Lys Arg Leu Lys Met Leu Gln Asp Pro Val	
205 210 215	

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24

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Cys Gly Glu Lys Lys Glu Val Asn Glu Gly Thr Lys Phe Glu Trp Leu	
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Glu Ser Ser Arg Ile Arg Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro	
235 240 245 250	
ctt tac gat aga aag acc tta cac ata cca cct gat gtt ttc aag aaa	939
Leu Tyr Asp Arg Lys Thr Leu His Ile Pro Pro Asp Val Phe Lys Lys	
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Met Ser Ala Ser Gln Lys Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met	
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Asp Ile Val Leu Phe Phe Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu	
285 290 295	
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Ser Gly Val Gly Lys Cys Arg Gln Val Gly Ile Ser Glu Ser Gly Ile	
315 320 325 330	
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Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys	
445 450 455	
gct cta agg aaa tat acg ttg aca ggg tct acg gcg gta cag ttg gct	1563
Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala	
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cca gta cca caa gta atg ggg gat aca gat gct gct gga gtt aga aat	1611
Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn	
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Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu	
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 685 690 695

ctt tat aaa ctc tgt aaa ctt cct ata tta gta gga aaa agc ggg cta 2283  
 Leu Tyr Lys Leu Cys Lys Leu Pro Ile Leu Val Gly Lys Ser Gly Leu  
 700 705 710

gag tta ttt ctt tct caa ttc gaa gca gcc ata gat agc gac ttt cca 2331  
 Glu Leu Phe Leu Ser Gln Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro  
 715 720 725 730

aat tat cag aac caa gat gtg aca gat gaa aac gct gaa act ctc aca 2379  
 Asn Tyr Gln Asn Gln Asp Val Thr Asp Glu Asn Ala Glu Thr Leu Thr  
 735 740 745

ata ctt atc gaa ctt ttt atc gaa aga gca act caa tgg tct gag gtc 2427  
 Ile Leu Ile Glu Leu Phe Ile Glu Arg Ala Thr Gln Trp Ser Glu Val  
 750 755 760

att cac acc ata agc tgc cta gat gtc ctg aga tct ttt gca atc gca 2475  
 Ile His Thr Ile Ser Cys Leu Asp Val Leu Arg Ser Phe Ala Ile Ala  
 765 770 775

gca agt ctc tct gct gga agc atg gcc agg cct gtt att ttt ccc gaa 2523  
 Ala Ser Leu Ser Ala Gly Ser Met Ala Arg Pro Val Ile Phe Pro Glu  
 780 785 790

tca gaa gct aca gat cag aat cag aaa aca aaa ggg cca ata ctt aaa 2571  
 Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys  
 795 800 805 810

atc caa gga cta tgg cat cca ttt gca gtt gca gcc gat ggt caa ttg 2619  
 Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu  
 815 820 825

cct gtt ccg aat gat ata ctc ctt ggc gag gct aga aga agc agt ggc 2667  
 Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly  
 830 835 840

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agc att cat cct cgg tca ttg tta ctg acg gga cca aac atg ggc gga 2715  
 Ser Ile His Pro Arg Ser Leu Leu Leu Thr Gly Pro Asn Met Gly Gly  
 845 850 855

aaa tca act ctt ctt cgt gca aca tgt ctg gcc gtt atc ttt gcc caa 2763  
 Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln  
 860 865 870

ctt ggc tgc tac gtg ccg tgt gag tct tgc gaa atc tcc ctc gtg gat 2811  
 Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp  
 875 880 885 890

act atc ttc aca agg ctt ggc gca tct gat aga atc atg aca gga gag 2859  
 Thr Ile Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Thr Gly Glu  
 895 900 905

agt acc ttt ttg gta gaa tgc act gag aca gcg tca gtt ctt cag aat 2907  
 Ser Thr Phe Leu Val Glu Cys Thr Glu Thr Ala Ser Val Leu Gln Asn  
 910 915 920

gca act cag gat tca cta gta atc ctt gac gaa ctg ggc aga gga act 2955  
 Ala Thr Gln Asp Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr  
 925 930 935

agt act ttc gat gga tac gcc att gca tac tcg gtt ttt cgt cac ctg 3003  
 Ser Thr Phe Asp Gly Tyr Ala Ile Ala Tyr Ser Val Phe Arg His Leu  
 940 945 950

gta gag aaa gtt caa tgt cgg atg ctc ttt gca aca cat tac cac cct 3051  
 Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro  
 955 960 965 970

ctc acc aag gaa ttc gcg tct cac cca cgt gtc acc tcg aaa cac atg 3099  
 Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met  
 975 980 985

gct tgc gca ttc aaa tca aga tct gat tat caa cca cgt ggt tgt gat 3147  
 Ala Cys Ala Phe Lys Ser Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp  
 990 995 1000

caa gac cta gtg ttc ttg tac cgt tta acc gag gga gct tgt cct gag 3195  
 Gln Asp Leu Val Phe Leu Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu  
 1005 1010 1015

agc tac gga ctt caa gtg gca ctc atg gct gga ata cca aac caa gtg 3243  
 Ser Tyr Gly Leu Gln Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val  
 1020 1025 1030

gtt gaa aca gca tca ggt gct gct caa gcc atg aag aga tca att ggg 3291  
 Val Glu Thr Ala Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly  
 1035 1040 1045 1050

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28

gga aac ttc aag tca agt gag cta aga tct gag ttc tca agt ctg cat 3339  
 Glu Asn Phe Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His  
 1055 1060 1065  
  
 gaa gac tgg ctc aag tca ttg gcg ggt att tct cga gtc gcc cac aac 3387  
 Glu Asp Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn  
 1070 1075 1080  
  
 aat gcc ccc att ggc gaa gat gac tac gac act ttg ttt tgc tta tgg 3435  
 Asn Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp  
 1085 1090 1095  
  
 cat gag atc aaa tcc tct tac tgt gtt ccc aaa taaatggcta 3478  
 His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys  
 1100 1105  
  
 tgacataaca ctatctgaag ctcggttaagt cttttgcctc tctgatgttt attcctctta 3538  
  
 aaaaatgctt atatatcaaa aaattgtttc ctcgattaaa aaaaaaaaaa aaaaaaaaaa 3598  
  
 aaaaaaaaaa 3606

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 1 5 10 15  
  
 Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly  
 20 25 30  
  
 Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly  
 35 40 45  
  
 Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg  
 50 55 60  
  
 Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser  
 65 70 75 80  
  
 Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser  
 85 90 95  
  
 Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly  
 100 105 110  
  
 Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys  
 115 120 125

004201-632250

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys  
 130 135 140  
 Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu  
 145 150 155 160  
 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu  
 165 170 175  
 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu  
 180 185 190  
 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn  
 195 200 205  
 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu  
 210 215 220  
 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg  
 225 230 235 240  
 Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr  
 245 250 255  
 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys  
 260 265 270  
 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe  
 275 280 285  
 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly  
 290 295 300  
 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys  
 305 310 315 320  
 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys  
 325 330 335  
 Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr  
 340 345 350  
 Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys  
 355 360 365  
 Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly  
 370 375 380  
 Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu  
 385 390 395 400  
 Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala  
 405 410 415

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Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala  
 420 425 430  
 Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp  
 435 440 445  
 Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr  
 450 455 460  
 Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met  
 465 470 475 480  
 Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly  
 485 490 495  
 Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu  
 500 505 510  
 Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His  
 515 520 525  
 Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe  
 530 535 540  
 Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met  
 545 550 555 560  
 Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly  
 565 570 575  
 Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg  
 580 585 590  
 Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile  
 595 600 605  
 Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser  
 610 615 620  
 Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg  
 625 630 635 640  
 Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu  
 645 650 655  
 Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe  
 660 665 670  
 Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala  
 675 680 685  
 Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys  
 690 695 700

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Leu	Pro	Ile	Leu	Val	Gly	Lys	Ser	Gly	Leu	Glu	Leu	Phe	Leu	Ser	Gln	
705						710					715					720
Phe	Glu	Ala	Ala	Ile	Asp	Ser	Asp	Phe	Pro	Asn	Tyr	Gln	Asn	Gln	Asp	
				725					730						735	
Val	Thr	Asp	Glu	Asn	Ala	Glu	Thr	Leu	Thr	Ile	Leu	Ile	Glu	Leu	Phe	
			740					745					750			
Ile	Glu	Arg	Ala	Thr	Gln	Trp	Ser	Glu	Val	Ile	His	Thr	Ile	Ser	Cys	
		755					760					765				
Leu	Asp	Val	Leu	Arg	Ser	Phe	Ala	Ile	Ala	Ala	Ser	Leu	Ser	Ala	Gly	
	770					775					780					
Ser	Met	Ala	Arg	Pro	Val	Ile	Phe	Pro	Glu	Ser	Glu	Ala	Thr	Asp	Gln	
785					790					795					800	
Asn	Gln	Lys	Thr	Lys	Gly	Pro	Ile	Leu	Lys	Ile	Gln	Gly	Leu	Trp	His	
				805					810						815	
Pro	Phe	Ala	Val	Ala	Ala	Asp	Gly	Gln	Leu	Pro	Val	Pro	Asn	Asp	Ile	
			820					825					830			
Leu	Leu	Gly	Glu	Ala	Arg	Arg	Ser	Ser	Gly	Ser	Ile	His	Pro	Arg	Ser	
		835					840					845				
Leu	Leu	Leu	Thr	Gly	Pro	Asn	Met	Gly	Gly	Lys	Ser	Thr	Leu	Leu	Arg	
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Ala	Thr	Cys	Leu	Ala	Val	Ile	Phe	Ala	Gln	Leu	Gly	Cys	Tyr	Val	Pro	
865					870					875					880	
Cys	Glu	Ser	Cys	Glu	Ile	Ser	Leu	Val	Asp	Thr	Ile	Phe	Thr	Arg	Leu	
				885					890					895		
Gly	Ala	Ser	Asp	Arg	Ile	Met	Thr	Gly	Glu	Ser	Thr	Phe	Leu	Val	Glu	
			900					905						910		
Cys	Thr	Glu	Thr	Ala	Ser	Val	Leu	Gln	Asn	Ala	Thr	Gln	Asp	Ser	Leu	
		915					920					925				
Val	Ile	Leu	Asp	Glu	Leu	Gly	Arg	Gly	Thr	Ser	Thr	Phe	Asp	Gly	Tyr	
	930					935					940					
Ala	Ile	Ala	Tyr	Ser	Val	Phe	Arg	His	Leu	Val	Glu	Lys	Val	Gln	Cys	
945					950					955					960	
Arg	Met	Leu	Phe	Ala	Thr	His	Tyr	His	Pro	Leu	Thr	Lys	Glu	Phe	Ala	
				965					970					975		
Ser	His	Pro	Arg	Val	Thr	Ser	Lys	His	Met	Ala	Cys	Ala	Phe	Lys	Ser	
			980					985					990			

32

Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu  
 995 1000 1005

Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val  
 1010 1015 1020

Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly  
 1025 1030 1035 1040

Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser  
 1045 1050 1055

Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser  
 1060 1065 1070

Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu  
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Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser  
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 microsatellite

<400> 32

accatgcata gcttaaactt cttg

24

<210> 33  
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 <212> DNA  
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<220>  
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<400> 33

acataaccac aaataggggt gc

22

00529239 102700



33

<210> 34  
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<400> 34  
 gaagcgatat tgttcgtg 18

<210> 35  
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 <223> Reverse primer DMCIN-B for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 35  
 agattgcgag aacattcc 18

<210> 36  
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 <223> Forward primer DMCIN-1 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 36  
 acgcgtcgac tcagctatga gattactcgt g 31

<210> 37  
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<400> 37  
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004201 6662550  
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<210> 38  
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<400> 38

gctctagagc ttctcttaag taagtgattg at 32

<210> 39  
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<400> 39

tcccccgggc tcgagagatc tccatgggtt cttcagctct atgaatcc 48

<210> 40  
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<220>  
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<400> 40

acgcgtcgac gaattcgcaa gtgggg 26

<210> 41  
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<212> DNA  
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<220>  
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<400> 41

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09529239 102700

tccatggaga tctccccgggt accgatttgc ttcgaggg

38

<210> 42  
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<220>  
 <223> Forward primer for PCR amplification of ATEAT1 SSLP marker in  
 Arabidopsis thaliana subspecies

<400> 42

gccactgcgt gaatgatatg

20

<210> 43  
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<220>  
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 Arabidopsis thaliana subspecies

<400> 43

cgaacagcca acattaattc cc

22

<210> 44  
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 <212> DNA  
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<220>  
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 Arabidopsis thaliana subspecies

<400> 44

aaccaaggca cagaagcg

18

<210> 45  
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<220>  
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 Arabidopsis thaliana subspecies

09529239.102700

<400> 45

acccaagtga tcgccacc

18

<210> 46

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<220>

<223> Forward primer for PCR amplification of NGA248 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 46

taccgaacca aaacacaaag g

21

<210> 47

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Reverse primer for PCR amplification of NGA248 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 47

tctgtatctc ggtgaattct cc

22

<210> 48

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of NGA128 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 48

ggtctgttga tgcgtaagt cg

22

<210> 49

<211> 22

<212> DNA

<213> Artificial sequence

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004204 66262560

<223> Reverse primer for PCR amplification of NGA128 SSLP marker in Arabidopsis thaliana subspecies

<400> 49

atcttgaaac ctttagggag gg 22

<210> 50

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies

<400> 50

ctgatctcac ggacaatagt gc 22

<210> 51

<211> 20

<212> DNA

<213> Artificial sequence

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<223> Reverse primer for PCR amplification of NGA280 SSLP marker in Arabidopsis thaliana subspecies

<400> 51

ggctccataa aaagtgcacc 20

<210> 52

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR amplification of NGA111 SSLP marker in Arabidopsis thaliana subspecies

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ctccagttgg aagctaaagg g 21

<210> 53

<211> 21

<212> DNA

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<220>  
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 <223> Forward primer for PCR amplification of NGA168 SSLP marker in  
 Arabidopsis thaliana subspecies  
  
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 ccttcacatc caaaacccac 20  
  
 <210> 55  
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 <212> DNA  
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 <223> Reverse primer for PCR amplification of NGA168 SSLP marker in  
 Arabidopsis thaliana subspecies  
  
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 <210> 56  
 <211> 20  
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 <223> Forward primer for PCR amplification of NGA1126 SSLP marker  
 in Arabidopsis thaliana subspecies  
  
 <400> 56  
 cgctacgctt ttcggtaaag 20

<210> 57  
<211> 20  
<212> DNA  
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<220>  
<223> Reverse primer for PCR amplification of NGA1126 SSLP marker  
in Arabidopsis thaliana subspecies

<400> 57

gcacagtcca agtcacaacc 20

<210> 58  
<211> 20  
<212> DNA  
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<220>  
<223> Forward primer for PCR amplification of NGA361 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 58

aaagagatga gaatttggac 20

<210> 59  
<211> 23  
<212> DNA  
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<220>  
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Arabidopsis thaliana subspecies

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acatatcaat atattaaagt agc 23

<210> 60  
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<212> DNA  
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<220>  
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Arabidopsis thaliana subspecies

<400> 60

004207-66262560

tcgtctactg cactgccg

18

<210> 61  
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Arabidopsis thaliana subspecies

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gaggacatgt ataggagcct cg

22

<210> 62  
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<220>  
<223> Forward primer for PCR amplification of AthBIO2 SSLP marker  
in Arabidopsis thaliana subspecies

<400> 62

tgacctcctc ttccatggag

20

<210> 63  
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<223> Reverse primer for PCR amplification of AthBIO2 SSLP marker  
in Arabidopsis thaliana subspecies

<400> 63

ttaacagaaa cccaaagctt tc

22

<210> 64  
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in Arabidopsis thaliana subspecies

09520239-102700



<400> 64  
aggcaaatgt ccatttcatt g 21

<210> 65  
<211> 20  
<212> DNA  
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<220>  
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in Arabidopsis thaliana subspecies

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acgacatggc agatttctcc 20

<210> 66  
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<220>  
<223> Forward primer for PCR amplification of NGA172 SSLP marker in  
Arabidopsis thaliana subspecies

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agctgcttcc ttatagcgtc c 21

<210> 67  
<211> 19  
<212> DNA  
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<220>  
<223> Reverse primer for PCR amplification of NGA172 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 67  
catccgaatg ccattgttc 19

<210> 68  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>

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<223> Forward primer for PCR amplification of NGA126 SSLP marker in  
Arabidopsis thaliana subspecies

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gaaaaaacgc tactttcgtg g

21

<210> 69

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of NGA126 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 69

caagagcaat atcaagagca gc

22

<210> 70

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for PCR amplification of NGA162 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 70

catgcaattt gcatctgagg

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<210> 71

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for PCR amplification of NGA162 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 71

ctctgtcact cttttcctct gg

22

<210> 72

<211> 21

<212> DNA

<213> Artificial sequence

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<220>  
<223> Forward primer for PCR amplification of NGA6 SSLP marker in  
Arabidopsis thaliana subspecies

<400> 72  
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<210> 73  
<211> 21  
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Arabidopsis thaliana subspecies

<400> 73  
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<210> 74  
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<220>  
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Arabidopsis thaliana subspecies

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